LifeSeq® Gold
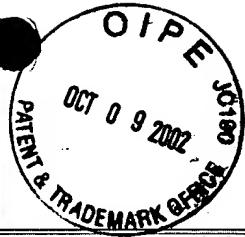Genomics for Life ™

BLAST2 Search Results

Main Menu	Genes	Libraries	Transcripts	Library Comp	Genomic Data	Sequences	Help

Retrieval	BLAST2	FASTA	ClustalW	GCG Assembly	Phrap	Translation	BLAST2 Manual

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Program: blastn
Sequence ID(s):

☐ 768320CB1 (LGcompseqsJAN2002) vs. gb129mam

NCBI-BLASTN 2.0.10 [Aug-26-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

Query= 768320CB1
        (1275 letters)

Database: gb129mam
          38,579 sequences; 40,433,150 total letters

Searching...done

	Sequences producing significant alignments:	Score (bits)	E Value
☑	g163228 Bovine inorganic pyrophosphatase mRNA sequence.	1227	0.0
☑	g9957596 Sus scrofa RNA helicase (RHIV-1) mRNA, complete cds.	38	0.16
☑	g6651078 Ovis aries proviral endogenous Jaagsiekte sheep retr	38	0.16
☑	g6851175 Ovis aries Jaagsiekte sheep retrovirus-like element,	36	0.64
☑	g6651074 Ovis aries proviral endogenous Jaagsiekte sheep retr	36	0.64

>g163228 Bovine inorganic pyrophosphatase mRNA sequence.
          Length = 1266

 Score = 1227 bits (619), Expect = 0.0
 Identities = 847/923 (91%)
 Strand = Plus / Plus

```
Query: 64   gcggcggcggcaggactccggcactatgagcggcttcagcaccgaggagcgcgccgcgcc 123
            ||||||||||| |  | |||||||| |||||| |||||||||| ||||||||||| |||||
Sbjct: 44   gcggcggcggctgttccccggcacgatgagcagcttcagcagcgaggagcgcgcggcgcc 103


Query: 124  cttctccctggagtaccgagtcttcctcaaaaatgagaaaggacaatatatatctccatt 183
            ||||  ||||| ||||||||||||||||||||||||| |||||||||||| ||| ||||||
Sbjct: 104  cttcaccctcgagtaccgagtcttcctcaaaaatgaaaaaggacaatatatctctccatt 163


Query: 184  tcatgatattccaatttatgcagataaggatgtgtttcacatggtagttgaagtaccacg 243
            |||||||||||||||||||||||||||||| |||||||||||||| |||||| |||| ||
Sbjct: 164  tcatgatattccaatttatgcagataaggaagtgtttcacatggtcgttgaagtgccgcg 223


Query: 244  ctggtctaatgcaaaaatggagattgctacaaaggacccctttaaaccctattaaacaaga 303
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                ||||||  |||||||||||||||||||||||||||||||||||||||| rrrrr |||||||||||
Sbjct: 224  ctggtcgaatgcaaaaatggagattgctacaaaggacccttttaaacccaattaaacaaga 283


Query: 304  tgtgaaaaaaggaaaacttcgctatgttgcgaatttgttcccgtataaaggatatatctg 363
                ||||||  |||||||||| || |||||||| ||| |||||||||||||||||| |||||
Sbjct: 284  tgtgaagaaaggaaaactccgttatgttgcaaatctgttcccgtataaaggatacatctg 343


Query: 364  gaactatggtgccatccctcagacttgggaagacccagggcacaatgataaacatactgg 423
                ||||||| |||||||||||||||||||||||||||||||| ||||||| |||||| |||||
Sbjct: 344  gaactacggtgccatccctcagacttgggaagacccaggacacaatgacaaacacactgg 403


Query: 424  ctgttgtggtgacaatgacccaattgatgtgtgtgaaattggaagcaaggtatgtgcaag 483
                |||||||||||||||||||||||||||||||||||||||||||||||||| |||||| |
Sbjct: 404  ctgttgtggtgacaatgacccaattgatgtgtgtgaaattggaagcaaggtgtgtgcacg 463


Query: 484  aggtgaaataattggcgtgaaagttctaggcatattggctatgattgacgaaggggaaac 543
                ||| || || || |  |||||||||| ||||| |||| ||||||||| |||||||| ||
Sbjct: 464  aggggagattatcagagtgaaagttctgggcattctggccatgattgatgaaggggagac 523


Query: 544  cgactggaaagtcattgccattaatgtggatgatcctgatgcagccaattataatgatat 603
                ||||||||||||||||||||||||||||||| |||||||||||||||||| ||||||||
Sbjct: 524  cgactggaaagtcattgccattaatgtggaagatcctgatgcagccaattacaatgatat 583


Query: 604  caatgatgtcaaacggctgaaacctggctacttagaagctactgtggactggtttagaag 663
                ||||||||||| ||||||||||||||||| | |||||||||||||||||| |||||||| ||
Sbjct: 584  taatgatgtcaagcggctgaaacctggctacctggaagctactgtggattggtttaggag 643


Query: 664  gtataaggttcctgatggaaaaccagaaaatgagtttgcgtttaatgcagaatttaaaga 723
                ||| |||||||| |||||||||| ||||||||||| ||||| || ||||||||||||||||
Sbjct: 644  gtacaaggttccagatggaaaacctgaaaatgagtttgctttcaatgcagaatttaaaga 703


Query: 724  taaggactttgccattgatattattaaaagcactcatgaccattggaaagcattagtgac 783
                |||| |||||||| ||||| ||||| |||||||||||||| |||||| ||||||||||||||
Sbjct: 704  taagaactttgcaattgacattattgaaagcactcatgactattggagagcattagtgac 763


Query: 784  taagaaaacgaatggaaaaaggaatcagttgcatgaatacaactttgtctgagagcccctt 843
                |||||||||  ||||||||||||||||| |||||||| || || ||||||||||||||||
Sbjct: 764  taagaaaactgatggaaaaaggaatcagctgcatgaacactacagtgtctgagagcccctt 823


Query: 844  caagtgtgatcctgatgctgccagagccattgtggatgctttaccaccaccctgtgaatc 903
                | |||||||||||||||||||||||| |||||||||||||||||||| ||||| ||||||||
Sbjct: 824  ccagtgtgatcctgatgctgccaaagccattgtggatgctttaccgccaccatgtgaatc 883


Query: 904  tgcctgcacagtaccaacagacgtggataagtggttccatcaccagaaaaactaatgaga 963
                |||||||||| |||||||||| ||||||||||||||||||||||||||||||||||| || |
Sbjct: 884  tgcctgcacaataccaacagatgtggataagtggttccatcaccagaaaaactaaggaaa 943


Query: 964  tttctctggaatacaagctgata 986
                |||||||||||||||||||||||
Sbjct: 944  tttctctggaatacaagctgata 966


  Score = 52.0 bits (26), Expect = 1e-05
  Identities = 32/34 (94%)
  Strand = Plus / Plus


Query: 1027  tagtagcttttcaaagctttaaatttgtagaact 1060
                 |||||||||||| |||||||||||||| |||||||
Sbjct: 1005  tagtagcttttccaagctttaaatttatagaact 1038
```

```
Score = 48.1 bits (24), Expect = 2e-04
Identities = 51/60 (85%)
Strand = Plus / Plus


Query: 1138 tcaactaagataactttttagcacatgcttaaatatcaaagcagttgtcatttggaagtca 1197
            |||||||||| |||| ||||| | ||||||||||||||| || ||||| ||||||||||||
Sbjct: 1108 tcaactaaggtaacatttagttcctgcttaaatatcaaggcggttgtagtttggaagtca 1167


>g9957596 Sus scrofa RNA helicase (RHIV-1) mRNA, complete cds.
           Length = 4024

 Score = 38.2 bits (19), Expect = 0.16
 Identities = 22/23 (95%)
 Strand = Plus / Plus


Query: 864  ccagagccattgtggatgcttta 886
            ||||||||| ||||||||||||||
Sbjct: 1961 ccagagcccttgtggatgcttta 1983


>g6651078 Ovis aries proviral endogenous Jaagsiekte sheep
           retrovirus-like clone enJSRV 5.9A1 protease (pro) gene,
           complete cds; and unknown gene.
           Length = 6696

 Score = 38.2 bits (19), Expect = 0.16
 Identities = 19/19 (100%)
 Strand = Plus / Plus


Query: 257  aaaatggagattgctacaa 275
            |||||||||||||||||||
Sbjct: 3378 aaaatggagattgctacaa 3396


>g6851175 Ovis aries Jaagsiekte sheep retrovirus-like element,
           complete sequence.
           Length = 7940

 Score = 36.2 bits (18), Expect = 0.64
 Identities = 18/18 (100%)
 Strand = Plus / Plus


Query: 258  aaatggagattgctacaa 275
            ||||||||||||||||||
Sbjct: 3398 aaatggagattgctacaa 3415


>g6651074 Ovis aries proviral endogenous Jaagsiekte sheep
           retrovirus-like clone enJSRV 5f16 Gag (gag), protease
           (pro), and envelope protein (env) genes, complete cds.
           Length = 6916

 Score = 36.2 bits (18), Expect = 0.64
 Identities = 18/18 (100%)
 Strand = Plus / Plus


Query: 258  aaatggagattgctacaa 275
            ||||||||||||||||||
Sbjct: 3398 aaatggagattgctacaa 3415


  Database: gb129mam
    Posted date:  May 6, 2002  5:07 PM
  Number of letters in database: 40,433,150
  Number of sequences in database:  38,579
```